

T. Wessendort

Re-run

1639



RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/840,277

DATE: 12/17/2002
TIME: 10:48:32

#10

Input Set : A:\A-688A.ST25.txt
Output Set: N:\CRF4\12172002\I840277.raw

RECEIVED

DEC 23 2002

TECH CENTER 1600/2900

3 <110> APPLICANT: FEIGE, ULRICH
4 KOHNO, TADAHIKO
5 LACEY, DAVID LEE
6 BOONE, THOMAS CHARLES
8 <120> TITLE OF INVENTION: INTEGRIN/ADHESION ANTAGONISTS
10 <130> FILE REFERENCE: A-688A
12 <140> CURRENT APPLICATION NUMBER: 09/840,277
13 <141> CURRENT FILING DATE: 2001-04-23
15 <150> PRIOR APPLICATION NUMBER: 60/198,919
16 <151> PRIOR FILING DATE: 2000-04-21
18 <150> PRIOR APPLICATION NUMBER: 60/201,394
19 <151> PRIOR FILING DATE: 2000-05-03
21 <160> NUMBER OF SEQ ID NOS: 135
23 <170> SOFTWARE: PatentIn version 3.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 684
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (1)..(684)
33 <223> OTHER INFORMATION:

W--> 36 <400> 1
37 atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg 48
38 Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
39 1 5 10 15
41 ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc 96
42 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
43 20 25 30
45 atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc 144
46 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
47 35 40 45
49 cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag 192
50 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
51 50 55 60
53 gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg 240
54 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
55 65 70 75 80
57 tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat 288
58 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
59 85 90 95
61 ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc 336
62 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro

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```

63          100          105          110
65 atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag      384
66 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
67          115          120          125
69 gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc      432
70 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
71          130          135          140
73 agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg      480
74 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
75 145          150          155          160
77 gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct      528
78 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
79          165          170          175
81 ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc      576
82 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
83          180          185          190
85 gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg      624
86 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
87          195          200          205
89 atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg      672
90 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
91          210          215          220
93 tct ccg ggt aaa      684
94 Ser Pro Gly Lys
95 225
98 <210> SEQ ID NO: 2
99 <211> LENGTH: 228
100 <212> TYPE: PRT
101 <213> ORGANISM: Homo sapiens
103 <400> SEQUENCE: 2
105 Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
106 1          5          10          15
109 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
110          20          25          30
113 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
114          35          40          45
117 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
118          50          55          60
121 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
122 65          70          75          80
125 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
126          85          90          95
129 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
130          100          105          110
133 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
134          115          120          125
137 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
138          130          135          140
141 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val

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```

142 145          150          155          160
145 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
146          165          170          175
149 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
150          180          185          190
153 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
154          195          200          205
157 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
158          210          215          220
161 Ser Pro Gly Lys
162 225
165 <210> SEQ ID NO: 3
166 <211> LENGTH: 8
167 <212> TYPE: PRT
168 <213> ORGANISM: Artificial Sequence
170 <220> FEATURE:
171 <223> OTHER INFORMATION: Preferred linker
173 <400> SEQUENCE: 3
175 Gly Gly Gly Lys Gly Gly Gly Gly
176 1          5
179 <210> SEQ ID NO: 4
180 <211> LENGTH: 8
181 <212> TYPE: PRT
182 <213> ORGANISM: Artificial Sequence
184 <220> FEATURE:
185 <223> OTHER INFORMATION: Preferred linker
187 <400> SEQUENCE: 4
189 Gly Gly Gly Asn Gly Ser Gly Gly
190 1          5
193 <210> SEQ ID NO: 5
194 <211> LENGTH: 8
195 <212> TYPE: PRT
196 <213> ORGANISM: Artificial Sequence
198 <220> FEATURE:
199 <223> OTHER INFORMATION: Preferred linker
201 <400> SEQUENCE: 5
203 Gly Gly Gly Cys Gly Gly Gly Gly
204 1          5
207 <210> SEQ ID NO: 6
208 <211> LENGTH: 5
209 <212> TYPE: PRT
210 <213> ORGANISM: Artificial Sequence
212 <220> FEATURE:
213 <223> OTHER INFORMATION: Preferred linker
215 <400> SEQUENCE: 6
217 Gly Pro Asn Gly Gly
218 1          5
221 <210> SEQ ID NO: 7
222 <211> LENGTH: 5

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223 <212> TYPE: PRT
224 <213> ORGANISM: Artificial Sequence
226 <220> FEATURE:
227 <223> OTHER INFORMATION: Laminin peptide
229 <400> SEQUENCE: 7
231 Tyr Ile Gly Ser Arg
232 1 5
235 <210> SEQ ID NO: 8
236 <211> LENGTH: 49
237 <212> TYPE: PRT
238 <213> ORGANISM: Artificial Sequence
240 <220> FEATURE:
241 <223> OTHER INFORMATION: Echistatin peptide
243 <400> SEQUENCE: 8
245 Glu Cys Glu Ser Gly Pro Cys Cys Arg Asn Cys Lys Phe Leu Lys Glu
246 1 5 10 15
249 Gly Thr Ile Cys Lys Arg Ala Arg Gly Asp Asp Met Asp Asp Tyr Cys
250 20 25 30
253 Asn Gly Lys Thr Cys Asp Cys Pro Arg Asn Pro His Lys Gly Pro Ala
254 35 40 45
257 Thr
261 <210> SEQ ID NO: 9
262 <211> LENGTH: 7
263 <212> TYPE: PRT
264 <213> ORGANISM: Artificial Sequence
266 <220> FEATURE:
267 <223> OTHER INFORMATION: RGD, NGR derivative peptide
269 <220> FEATURE:
270 <221> NAME/KEY: misc_feature
271 <222> LOCATION: (2, 5 and)..(7)
272 <223> OTHER INFORMATION: Xaa is any amino acid
275 <400> SEQUENCE: 9
W--> 277 Arg Xaa Glu Thr Xaa Trp Xaa
278 1 5
281 <210> SEQ ID NO: 10
282 <211> LENGTH: 7
283 <212> TYPE: PRT
284 <213> ORGANISM: Artificial Sequence
286 <220> FEATURE:
287 <223> OTHER INFORMATION: RGD, NGR derivative peptide
289 <220> FEATURE:
290 <221> NAME/KEY: misc_feature
291 <222> LOCATION: (2, 5 and)..(7)
292 <223> OTHER INFORMATION: Xaa is any amino acid
295 <400> SEQUENCE: 10
W--> 297 Arg Xaa Glu Thr Xaa Trp Xaa
298 1 5
301 <210> SEQ ID NO: 11
302 <211> LENGTH: 9

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303 <212> TYPE: PRT
304 <213> ORGANISM: Artificial Sequence
306 <220> FEATURE:
307 <223> OTHER INFORMATION: RGD, NGR derivative peptide
309 <220> FEATURE:
310 <221> NAME/KEY: misc_feature
311 <222> LOCATION: (2, 3, 7 and)..(8)
312 <223> OTHER INFORMATION: Xaa is any amino acid
315 <400> SEQUENCE: 11
W--> 317 Cys Xaa Xaa Arg Leu Asp Xaa Xaa Cys
318 1 5
321 <210> SEQ ID NO: 12
322 <211> LENGTH: 7
323 <212> TYPE: PRT
324 <213> ORGANISM: Artificial Sequence
326 <220> FEATURE:
327 <223> OTHER INFORMATION: RGD, NGR derivative peptide
329 <220> FEATURE:
330 <221> NAME/KEY: misc_feature
331 <222> LOCATION: (2 and)..(3)
332 <223> OTHER INFORMATION: Xaa is any amino acid
335 <400> SEQUENCE: 12
W--> 337 Cys Xaa Xaa Arg Gly Asp Cys
338 1 5
341 <210> SEQ ID NO: 13
342 <211> LENGTH: 9
343 <212> TYPE: PRT
344 <213> ORGANISM: Artificial Sequence
346 <220> FEATURE:
347 <223> OTHER INFORMATION: RGD, NGR derivative peptide
349 <220> FEATURE:
350 <221> NAME/KEY: misc_feature
351 <222> LOCATION: (1, 2, 3, 7, 8 and)..(9)
352 <223> OTHER INFORMATION: Xaa is any amino acid
355 <400> SEQUENCE: 13
W--> 357 Xaa Xaa Xaa Arg Gly Asp Xaa Xaa Xaa
358 1 5
361 <210> SEQ ID NO: 14
362 <211> LENGTH: 9
363 <212> TYPE: PRT
364 <213> ORGANISM: Artificial Sequence
366 <220> FEATURE:
367 <223> OTHER INFORMATION: RGD, NGR derivative peptide
369 <220> FEATURE:
370 <221> NAME/KEY: misc_feature
371 <222> LOCATION: (2 )..(8)
372 <223> OTHER INFORMATION: Xaa is any amino acid
376 <400> SEQUENCE: 14
W--> 378 Cys Xaa Cys Arg Gly Asp Cys Xaa Cys

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; Xaa Pos. 2,5,7
Seq#:10; Xaa Pos. 2,5,7
Seq#:11; Xaa Pos. 2,3,7,8
Seq#:12; Xaa Pos. 2,3
Seq#:13; Xaa Pos. 1,2,3,7,8,9
Seq#:14; Xaa Pos. 2,8
Seq#:15; Xaa Pos. 1,2,5,6,7,8
Seq#:16; Xaa Pos. 1,2,3,6,7,8,9,10
Seq#:17; Xaa Pos. 3,5,6,13,15
Seq#:18; Xaa Pos. 2,3,4,7,15
Seq#:19; Xaa Pos. 3,4,5,6,8,13,15,18
Seq#:20; Xaa Pos. 2,5,6,7,12,13,14
Seq#:21; Xaa Pos. 1,3,6,9,12,13
Seq#:40; Xaa Pos. 3,4
Seq#:50; Xaa Pos. 2,3
Seq#:58; Xaa Pos. 5
Seq#:59; Xaa Pos. 6
Seq#:86; Xaa Pos. 3,15
Seq#:87; Xaa Pos. 13,15

VERIFICATION SUMMARY

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Input Set : A:\A-688A.ST25.txt

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L:36 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:33
L:277 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:297 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:317 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:337 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:357 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:378 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
L:410 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:448 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
L:468 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
L:492 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
L:512 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
L:516 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:16
L:536 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0
L:556 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0
L:828 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40 after pos.:0
L:974 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50 after pos.:0
L:1120 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:0
L:1140 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59 after pos.:0
L:1536 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:86 after pos.:0
L:1556 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:87 after pos.:0
L:1878 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:108,Line#:1869